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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/805,550

DATE: 03/27/2001
 TIME: 16:06:01

Input Set : A:\0964D sequence listing.txt
 Output Set: N:\CRF3\03272001\I805550.raw

ENTERED

4 <110> APPLICANT: Mahajan, Pramod B.
 5 Tagliani, Laura
 7 <120> TITLE OF INVENTION: Rad23 Genes and Uses Thereof
 10 <130> FILE REFERENCE: 0964D
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/805,550
 C--> 12 <141> CURRENT FILING DATE: 2001-03-13
 12 <150> PRIOR APPLICATION NUMBER: 09/413,574
 13 <151> PRIOR FILING DATE: 1999-10-06
 15 <150> PRIOR APPLICATION NUMBER: 60/109,728
 16 <151> PRIOR FILING DATE: 1998-11-23
 18 <160> NUMBER OF SEQ ID NOS: 5
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1522
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Zea mays
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (58)...(1272)
 31 <400> SEQUENCE: 1
 32 cgaccacgc gtccggtgag gaggtagagt tcaaggaccg aggcggcgctc gggcgag atg 60
 33 Met
 34 1
 36 aag ctt aac gtc aag acc ctc aag ggc acc aac ttc gag atc gag gcg 108
 37 Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu Ala
 38 5 10 15
 40 agc ccc gat gca tcg gtt gct gat gtg aag agg atc att gag acc act 156
 41 Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr Thr
 42 20 25 30
 44 caa ggt cag agt acc tac cgg gcg gac cag caa atg ctc ata tac caa 204
 45 Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr Gln
 46 35 40 45
 48 ggg aaa att ctc aag gat gaa acc act ttg gaa agc aac gga gtt gct 252
 49 Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val Ala
 50 50 55 60 65
 52 gag aac agc ttc ctt gtt ata atg ttg tcc aag gct aag gca tca tcg 300
 53 Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser Ser
 54 70 75 80
 56 agt gga gct tct acc gct act act gca aaa gct cct gca act ctg gcc 348
 57 Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu Ala
 58 85 90 95
 60 caa cct gct gcc cct gtg gcc cct gct gca tca gtt gca aga aca cca 396
 61 Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr Pro
 62 100 105 110
 65 aca cag gct cct gtt gcc aca gct gaa acg gca cct cca agt gtc caa 444
 66 Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Val Gln
 67 115 120 125

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69	cct cag gct gct cca gct gct acg gtt gct gct act gat gat gct gat	492
70	Pro Gln Ala Ala Pro Ala Ala Thr Val Ala Ala Thr Asp Asp Ala Asp	
71	130 135 140 145	
73	gtg tac agt cag gca gct tca aac ctt gta ttt ggc aac aat cta gaa	540
74	Val Tyr Ser Gln Ala Ala Ser Asn Leu Val Phe Gly Asn Asn Leu Glu	
75	150 155 160	
77	cag act atc caa caa att ctt gac atg ggt ggt ggt aca tgg gaa cgt	588
78	Gln Thr Ile Gln Gln Ile Leu Asp Met Gly Gly Gly Thr Trp Glu Arg	
79	165 170 175	
81	gat act gtt gtt cgt gct cta cgt gct gca tac aat aac ccc gag aga	636
82	Asp Thr Val Val Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu Arg	
83	180 185 190	
85	gct ata gac tac ctg tat tct gga att cct gag aat gtg gag gct cag	684
86	Ala Ile Asp Tyr Leu Tyr Ser Gly Ile Pro Glu Asn Val Glu Ala Gln	
87	195 200 205	
89	cct gtt gcc cga gca cct gct gct ggc caa caa aca aat cag cag gcc	732
90	Pro Val Ala Arg Ala Pro Ala Ala Gly Gln Gln Thr Asn Gln Gln Ala	
91	210 215 220 225	
93	gca tca ccc gct cag cca gca gtt gca ttg cca gtg cag cca tca cct	780
94	Ala Ser Pro Ala Gln Pro Ala Val Ala Leu Pro Val Gln Pro Ser Pro	
95	230 235 240	
97	gcc tct gca ggg cct aat gca aat cct ttg aac ctt ttt cct cag ggt	828
98	Ala Ser Ala Gly Pro Asn Ala Asn Pro Leu Asn Leu Phe Pro Gln Gly	
99	245 250 255	
101	gtt cca agt ggt ggg tcc aac cca ggt gtt gtt cca ggt gca gga tct	876
102	Val Pro Ser Gly Gly Ser Asn Pro Gly Val Val Pro Gly Ala Gly Ser	
103	260 265 270	
105	ggt gct ctt gat gcc ttg cga cag ctt cca cag ttt caa gca ctc ctt	924
106	Gly Ala Leu Asp Ala Leu Arg Gln Leu Pro Gln Phe Gln Ala Leu Leu	
107	275 280 285	
109	cag tta gtc cag gct aat cct caa atc ttg cag cca atg ctt caa gag	972
110	Gln Leu Val Gln Ala Asn Pro Gln Ile Leu Gln Pro Met Leu Gln Glu	
111	290 295 300 305	
113	cta ggt aaa caa aac cca caa att ctg cgg ttg att cag gaa aat caa	1020
114	Leu Gly Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Gln Glu Asn Gln	
115	310 315 320	
117	gct gag ttt ctc cgc ttg gtg aat gaa tct cct gag ggt ggt cct gga	1068
118	Ala Glu Phe Leu Arg Leu Val Asn Glu Ser Pro Glu Gly Gly Pro Gly	
119	325 330 335	
121	ggg aac ata cta ggt caa ctg gca gct gct gtg cca caa acg ctg aca	1116
122	Gly Asn Ile Leu Gly Gln Leu Ala Ala Ala Val Pro Gln Thr Leu Thr	
123	340 345 350	
127	gtt acc cca gag gaa cgg gag gct atc cag cgg ctc gag gga atg ggg	1164
128	Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met Gly	
129	355 360 365	
131	ttc aac cgt gag ctt gtg cta gaa gtt ttc ttt gca tgc aac aag gac	1212
132	Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys Asp	
133	370 375 380 385	
135	gaa gag ctt aca gcc aac tac ctc ctg gat cat ggc cat gag ttt gac	1260

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136  Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe Asp
137                      390                      395                      400
139  gat cag cag caa tagacgtggg gtggatggag gaaaccgagg cagttgcaga      1312
140  Asp Gln Gln Gln
141                      405
143  acagcgagtg tcgttcttat gccctctgcc tgacgagaga tactcggtcg tctatgctat      1372
144  gctgctgact atcttttatt tccatatata ttgttcgga atgctttcta agtacatatt      1432
145  aattcaatat caagcggttac accgtgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1492
146  aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1522
148  <210> SEQ ID NO: 2
149  <211> LENGTH: 405
150  <212> TYPE: PRT
151  <213> ORGANISM: Zea mays
153  <400> SEQUENCE: 2
154  Met Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu
155  1          5          10          15
156  Ala Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr
157  20          25          30
158  Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr
159  35          40          45
160  Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val
161  50          55          60
162  Ala Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser
163  65          70          75          80
164  Ser Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu
165  85          90          95
166  Ala Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr
167  100         105         110
168  Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Val
169  115         120         125
170  Gln Pro Gln Ala Ala Pro Ala Ala Thr Val Ala Ala Thr Asp Asp Ala
171  130         135         140
172  Asp Val Tyr Ser Gln Ala Ala Ser Asn Leu Val Phe Gly Asn Asn Leu
173  145         150         155         160
174  Glu Gln Thr Ile Gln Gln Ile Leu Asp Met Gly Gly Gly Thr Trp Glu
175  165         170         175
176  Arg Asp Thr Val Val Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu
177  180         185         190
178  Arg Ala Ile Asp Tyr Leu Tyr Ser Gly Ile Pro Glu Asn Val Glu Ala
179  195         200         205
180  Gln Pro Val Ala Arg Ala Pro Ala Ala Gly Gln Gln Thr Asn Gln Gln
181  210         215         220
182  Ala Ala Ser Pro Ala Gln Pro Ala Val Ala Leu Pro Val Gln Pro Ser
183  225         230         235         240
184  Pro Ala Ser Ala Gly Pro Asn Ala Asn Pro Leu Asn Leu Phe Pro Gln
185  245         250         255
186  Gly Val Pro Ser Gly Gly Ser Asn Pro Gly Val Val Pro Gly Ala Gly
187  260         265         270
189  Ser Gly Ala Leu Asp Ala Leu Arg Gln Leu Pro Gln Phe Gln Ala Leu

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DATE: 03/27/2001

PATENT APPLICATION: US/09/805,550

TIME: 16:06:01

Input Set : A:\0964D sequence listing.txt

Output Set: N:\CRF3\03272001\I805550.raw

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190          275          280          285
191 Leu Gln Leu Val Gln Ala Asn Pro Gln Ile Leu Gln Pro Met Leu Gln
192          290          295          300
193 Glu Leu Gly Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Gln Glu Asn
194 305          310          315          320
195 Gln Ala Glu Phe Leu Arg Leu Val Asn Glu Ser Pro Glu Gly Gly Pro
196          325          330          335
197 Gly Gly Asn Ile Leu Gly Gln Leu Ala Ala Val Pro Gln Thr Leu
198          340          345          350
199 Thr Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met
200          355          360          365
201 Gly Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys
202          370          375          380
203 Asp Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe
204 385          390          395          400
205 Asp Asp Gln Gln Gln
206          405
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 1702
210 <212> TYPE: DNA
211 <213> ORGANISM: Zea mays
213 <220> FEATURE:
214 <221> NAME/KEY: CDS
215 <222> LOCATION: (106)...(1209)
217 <400> SEQUENCE: 3
218 ccagccaccc gtaaaaccct agacggctag ccgcgcacgg aagcgggcag cggagcggag 60
219 gtgagcctct cctgcatcgg attgtccccg ccccgctag gcgcc atg aag ctg acg 117
220 Met Lys Leu Thr
221 1
223 gtg aag acc ctc aag gga acg cac ttc gag atc cgg gtg cag ccc aac 165
224 Val Lys Thr Leu Lys Gly Thr His Phe Glu Ile Arg Val Gln Pro Asn
225 5 10 15 20
227 gac acg att atg gct gtg aag aag aat ata gaa gag ata caa ggg aaa 213
228 Asp Thr Ile Met Ala Val Lys Lys Asn Ile Glu Glu Ile Gln Gly Lys
229 25 30 35
231 gac agc tat cca tgg ggc caa caa ctg ctg att ttc aat gga aag gtc 261
232 Asp Ser Tyr Pro Trp Gly Gln Gln Leu Leu Ile Phe Asn Gly Lys Val
233 40 45 50
235 ttg aaa gat gaa agt aca ttg gaa gag aat aaa gtc aat gag gat ggg 309
236 Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val Asn Glu Asp Gly
237 55 60 65
239 ttt cta gtt gtc atg ctt agt aag ggt aaa aca tct ggt tca act gga 357
240 Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser Gly Ser Thr Gly
241 70 75 80
243 act tca tct tcc cag cac tca aac act cct gca aca agg cag gca cct 405
244 Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr Arg Gln Ala Pro
245 85 90 95 100
247 cct cta gag gcc cca caa caa gct cct caa ccc ccg gtg gca cca att 453
248 Pro Leu Glu Ala Pro Gln Gln Ala Pro Gln Pro Pro Val Ala Pro Ile

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TIME: 16:06:01

Input Set : A:\0964D sequence listing.txt

Output Set: N:\CRF3\03272001\I805550.raw

249		105		110		115		
251	aca act tct cag cct gaa gga ctt cct gca cag gca cct aac aca cat							501
252	Thr Thr Ser Gln Pro Glu Gly Leu Pro Ala Gln Ala Pro Asn Thr His							
253		120		125		130		
255	gac aat gcg gca tca aat ctt ctg tct gga agg aat gtt gac aca ata							549
256	Asp Asn Ala Ala Ser Asn Leu Leu Ser Gly Arg Asn Val Asp Thr Ile							
257		135		140		145		
259	att aac cag cta atg gag atg ggt ggg ggc agt tgg gac aaa gat aaa							597
260	Ile Asn Gln Leu Met Glu Met Gly Gly Gly Ser Trp Asp Lys Asp Lys							
261		150		155		160		
263	gtc caa agg gct ctc cgt gcc gct tac aac aac ccc gaa cgt gct gtt							645
264	Val Gln Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu Arg Ala Val							
265	165		170		175		180	
267	gaa tac ctc tac tct ggt att cca gta aca gct gaa att gct gtt cca							693
268	Glu Tyr Leu Tyr Ser Gly Ile Pro Val Thr Ala Glu Ile Ala Val Pro							
269		185		190		195		
271	att ggt ggt caa ggg gca aac aca act gat cga gct cct act ggg gaa							741
272	Ile Gly Gly Gln Gly Ala Asn Thr Thr Asp Arg Ala Pro Thr Gly Glu							
273		200		205		210		
275	gct ggt ctc tct ggg att cca aac acc gct cca cta gat ctt ttc ccg							789
276	Ala Gly Leu Ser Gly Ile Pro Asn Thr Ala Pro Leu Asp Leu Phe Pro							
277		215		220		225		
279	cag ggg gct tcc aat gct gga ggt ggt gct ggt ggt gga cca ctt gat							837
280	Gln Gly Ala Ser Asn Ala Gly Gly Gly Ala Gly Gly Pro Leu Asp							
281		230		235		240		
283	ttt ctt aga aac aat cca cag ttt caa gca gtt agg gaa atg gtc cat							885
284	Phe Leu Arg Asn Asn Pro Gln Phe Gln Ala Val Arg Glu Met Val His							
285	245		250		255		260	
287	aca aat cca caa att ttg cag cct atg ctc gtt gag ttg agc aag cag							933
288	Thr Asn Pro Gln Ile Leu Gln Pro Met Leu Val Glu Leu Ser Lys Gln							
289		265		270		275		
291	aat cct caa att cta agg ttg att gag gag aat cat gat gag ttt ctt							981
292	Asn Pro Gln Ile Leu Arg Leu Ile Glu Glu Asn His Asp Glu Phe Leu							
293		280		285		290		
295	cag tta cta aat gag ccc ttt gaa ggc gga gag ggg gat ttc tta gac							1029
296	Gln Leu Leu Asn Glu Pro Phe Glu Gly Gly Glu Gly Asp Phe Leu Asp							
297		295		300		305		
299	caa cct gag gag gat gaa atg cct cat gcc att agt gtt aca cca gag							1077
300	Gln Pro Glu Glu Asp Glu Met Pro His Ala Ile Ser Val Thr Pro Glu							
301		310		315		320		
303	gag cag gag gcc att gga cgg ctt gag tcc atg ggg ttc gac aga gca							1125
304	Glu Gln Glu Ala Ile Gly Arg Leu Glu Ser Met Gly Phe Asp Arg Ala							
305		325		330		335		340
307	cgc gtt att gaa gca ttc tta gcc tgc gat agg aac gag gag cta gca							1173
308	Arg Val Ile Glu Ala Phe Leu Ala Cys Asp Arg Asn Glu Glu Leu Ala							
309		345		350		355		
313	gca aac tat ctc ctt gag cat gct ggt gag gaa gat taagcgggag							1219
314	Ala Asn Tyr Leu Leu Glu His Ala Gly Glu Glu Asp							
315		360		365				

VERIFICATION SUMMARY DATE: 03/27/2001
PATENT APPLICATION: US/09/805,550 TIME: 16:06:02

Input Set : A:\0964D sequence listing.txt
Output Set: N:\CRF3\03272001\I805550.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date